Strong protein sequence alignment between autoantigens involved in cardiac arrhythmias and vaccine antigens

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Background

Autoantibodies against proteins encoded by CACNA1C, CACNA1S, CACNA1D, CACNA1F, SCN5A, TRIM21, K_VLQT1 α, KCNH2 and KCNA4 have been associated with cardiac arrhythmias[1].

The origin of these autoantibodies is unknown. We know from Pandemrix vaccine induced narcolepsy,[2] that vaccine antigens can induce autoimmunity due to molecular mimicry. Protein sequence alignment between these autoantigens and vaccine antigens or contaminants was examined to check if the autoantibodies could have been induced by vaccines.

Method

Protein sequences for the autoantigens were obtained from Uniprot.[3]

BLASTP methodology was used for protein sequence alignment.

As shown before[4], a BLASTP sequence alignment score of 19.3 was obtained comparing human hypocretin receptor and H1N1 nucleoprotein contained in the Pandemrix vaccine. This level of sequence alignment was sufficient to cause autoimmunity that resulted in hypocretin dysregulation and narcolepsy.[2] Therefore any score equal to or higher than 19.3 suggests high probability of autoimmunity.

While vaccines target one or a few particular viral/bacterial proteins, most vaccines are contaminated with all proteins from the virus or bacteria. Example: the Pandemrix vaccine contained both H1N1 hemagglutinin (target) and H1N1 nucleoproteins (contaminant). The exceptions are recombinant vaccines. In recombinant vaccines, the vaccine contains only the target protein from the target organism. The target protein is produced usually by genetically modifying yeast (Saccharomyces cerevisiae). Hepatitis B[5,6] and HPV vaccines[7] are produced using this technique. Such vaccines are however, contaminated with all Saccharomyces cerevisiae proteins.

Results

The table below shows sequence alignment scores between autoantigens and vaccine antigens. A score equal to or greater than 19.3 indicates high probability of inducing cross-reacting autoantibodies following vaccination.

Autoantigen	CACNA1C	CACNA1S	CACNA1D	CACNA1F	SCN5A	TRIM21	K_vLQT1 α	KCNH2	KCNA4
Vaccine Antigen									
Saccharomyces cerevisiae	192	172	67.4	146	70.9	39.7		33.5	27.3
Streptococcus pneumoniae	53.1	62.8	71.2	53.1	69.7		62.4	55.1	91.7
Corynebacterium diphtheriae	27.3	32.3	25.8	28.5	26.6	29.6	26.2	37.4	37.4
Bordetella pertussis	28.5		28.9	34.7	31.6	30	38.1	44.7	39.3
Clostridium tetani	29.3	25	25	25	35.8	31.6	23.5	29.6	
Neisseria meningitidis	30.4	27.7	28.5	27.7	28.1	29.6	27.3	26.9	30
Haemophilus influenzae	26.9	27.7	26.9	31.2	32	24.6	27.7	44.3	26.2
Hepatitis B	33.5	32	29.3		27.3		24.3		
Rubella							20.4		
Influenza A									26.6
Hepatitis A			31.2						

Discussion

The results above show strong sequence alignment between many autoantigens and vaccine antigens. Therefore there is a high probability that these autoantibodies were induced as a result of vaccination.

Most vaccines involve injecting viral or bacterial proteins as an intramuscular injection. The route of exposure during natural infection by these viruses and bacteria is usually through the eyes, nose or mouth and not intramuscular injection. We have evolved immune mechanisms specific to routes of exposure and specific to pathogens. Examples include skin-homing versus gut-homing immune cells produced by different lymph nodes.[8] Pathogen Associated Molecular Patterns (PAMP) or Danger Associated Molecular Patterns (DAMP) recognized by pattern recognition receptors (PRR) expressed on dendritic cells (DC). Aluminum adjuvanted vaccines artificially boost and induce immune responses to viral, bacterial antigens introduced through an artificial route of exposure. This completely disrupts the natural immune response to the vaccine antigens by activating immune pathways quite different from the pathways involved during natural infection. Therefore, protections against autoimmunity during natural infection which have evolved over millions of years, are bypassed in the case of vaccine induced immune responses.

One can therefore logically expect a skewed immune response which could include autoimmunity as was demonstrated in the case of Pandemrix vaccine induced narcolepsy. Pandemrix vaccine contained H1N1 viral proteins along with squalene as an adjuvant.

Similarly, with aluminum adjuvanted vaccines that artificially boost immune response to weakly immunogenic vaccine antigens, the natural protection against autoimmunity can be disrupted.[9]

Dr. François Verdier, an immunotoxicology expert with vaccine maker Aventis Pasteur (now Sanofi Pasteur) wrote in Biotechnology and Safety Assessment (2003)[10]:

“Advances in computer software such as LifeSeq from Incyte and the availability of the human genome sequence allow rapid comparison between the protein sequence alignment of a vaccine antigen and a host protein.”

He also explains that this can catch primary structure mimicry but may miss conformational mimicry. He recommends, “From these hypothesises (sic), a recommended strategy would be to avoid any vaccine antigen presenting a mimicry with a host antigen involved in an autoimmune disease.”

A recommendation the vaccine industry has mostly ignored, resulting in devastating consequences.

Genetic susceptibility

The efficiency of producing autoimmunity in the presence of molecular mimicry could of course be influenced by genetic variations. So it may be possible to identify genetic markers for such susceptibility. While such identification would be interesting, the root cause, vaccines, need to be fixed.

Action

All vaccine design aspects including removal of contaminating proteins[11], handling molecular mimicry and route of administration need to be revisited to avoid such off-target immune responses.

Detailed Results

Voltage-dependent L-type calcium channel subunit alpha-1C (CACNA1C)

Cch1p [Saccharomyces cerevisiae YJM270]
AJR78792.1 2039 2

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
192 bits(489)	3e-47	Compositional matrix adjust.	239/1063(22%)	434/1063(40%)	167/1063(15%)

```
Query  625   LRIFKITRYWNSL------SNLVASLLNSVRSIASLLLLLFLFIIIFSLLGMQLFGGKFN  678
                 L IF I+R++  +       L   +L++   I +L    F F  + +++    F G
Sbjct  866   LSIFHISRFYRVIISFKLTKKLWKQILSNGVMIWNLSSFYFFFTFLVAIIMAVYFEGVIP  925

Query  679   FDEMQTRRSTFDNFPQSLLTVFQILTGEDWNSVMYDGIMAYGGPSFPGMLVC-IYFIILF  737
                   +EM  +     + P S L++F I + E+W  ++Y   +    P+      C ++FII F
Sbjct  926   PEEMADQPFGMYSLPNSFLSLFIIGSTENWTDILY--ALQKHSPNISSTFFCSVFFIIWF  983

Query  738   ICGNYILLNVFLAIAVDNLADAESLTSAQKEEEEEKERKKLARTASPEKKQELVEKPAV-  796
                   +  N ++LN+F+A+  +++         ++EE+  ++ K   +  P+K QE      V
Sbjct  984   LLSNSVILNIFIALISESM-------EVKEEEKRPQQIKHYLKFVYPQKIQEYTHASLVA  1036

Query  797   --------GESKEEKIELKSITADGESPPATKINMDDLQ------PNENEDKSP------  836
                              G   E+  + K     G +      NM +L       P+EN  K
Sbjct  1037  RIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFKEPPSENLFKKGLSKLTI  1096

Query  837   ----------------YPNPETTGEEDEEEPEMPVGPRPRPLSELHLKE-------KAVP  873
                                          Y N +    E +     + R   L EL+  E       K  P
Sbjct  1097  GVPSLKRLRMFANNPFYKNSDVVFTETND-----INGRTYIL-ELNEYEDEKLDYLKKYP  1150

Query  874   MPEASAFFIFSSNNRFRLQCHRIVNDTI--FTNLILFFILLSSISLAAEDPVQHTSFRNH  931
                   +   S +F FS  +RFR  C R+V  +    T+   FF         + D     S+ +H
Sbjct  1151  LFNYSYYF-FSPQHRFRRFCQRLVPPSTGKRTDGSRFF-------EDSTDLYNKRSYFHH  1202

Query  932   I---LFYFDIVFTTIFTIEIALKI---------LGN------ADYVFTSIFTLEIILKMT  973
                   I   +F F     TI  I  +  +         +G        D  F   F++E I+K
Sbjct  1203  IERDVFVFIFALATILLIVCSCYVTPLYRMHHKMGTWNWSSALDCAFIGAFSIEFIVKTV  1262

Query  974   AYGAFLHKGSFCRNYFNILD---LLVVSVSLISFGIQSSAINVVKILRVLRVLRPLRAIN  1030
                   A G      ++ RN +N +D   L+ + ++LI++   +   N+ +I + L  LR LR +
Sbjct  1263  ADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNG--NLSRIFKGLTALRALRCLT  1320

Query  1031  RAKGLKHVVQCV-FVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLYTCSDSSKQTEAEC  1089
                     +   +    V F  + I    +++  L F F   G+ +FKG+L TC+D S    A+C
Sbjct  1321  ISNTARQTFNLVMFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRLGTCNDGS-LGRADC  1379

Query  1090  KGNYITYKDGEVDHPIIQPRSWENSKFDFDNVLAAMMALFTVSTFEGWPELLYRSIDSHT  1149
                         Y  Y +      I+ PR ++      D+  +A  +L+ + + EGW +LL   ++S
Sbjct  1380  ---YNEYSNSVFQWDIMSPRVYQQPYLHLDSFASAFNSLYQIISLEGWVDLLENMMNSSG  1436

Query  1150  EDKGPIYNYRVEISIFFIIYIIIIAFFMMNIFVGFVIVTFQEQGEQEYKNCELDKNQRQC  1209
                                        ++F +++I +   F++N+FV F++          Y   E +K   +
Sbjct  1437  IGTPATVMGSAGNALFLVLFIFLSMVFILNLFVSFIVNNQARTTGSAYFTIE-EKAWLES  1495
```

```
Query  1210  VEYALKARPLRRYIPK-------NQHQYKVWYVVNSTYFEYLMFVLILLNTICLAMQHYG  1262
                    +   +A+P  + IP        Q  Y++     + Y+   + V++ L+ I L  + Y
Sbjct  1496  QKLLSQAKP--KAIPNLIELSRVRQFFYQLAVEKKNFYYASFLQVVLYLHIIMLLSRSYN  1553

Query  1263  QSCLFKIAMNILNMLFTGLFTVEMILKLIAFKPKGYFSDPWNVFDFLIVIGSIIDVILSE  1322
                       L      +  M  T +F ++  L +    P+ YF   WN
Sbjct  1554  PGNLIG-YQGVYFMFSTSVFLIQEALHMCGEGPRLYFRQKWNSIRL----------  1598

Query  1323  TNHYFCDAWNTFDALIVVGSIVDIAITEVNPAEHTQCSPSMNAEENSRISITFFRLFRVM  1382
                                        ++I++  I++     V PA H             +I  F L  +
Sbjct  1599  -------------SIIIIAFIMNAVAFHV-PASHYWFH-----------NIKGFFLLVIF  1633

Query  1383  RLVKLLSRGEGIRTLLWTFIKSFQALPYVALLIVMLFFIYAVIGMQVFGKIALNDTTEIN  1442
                       +  + + + +  LL T + S   +  +     +LF +YA+   Q+FG   L   T
Sbjct  1634  LFI--IPQNDTLTELLETAMASLPPILSLTYTWGVLFLVYAIALNQIFGLTRLGSNT--T  1689

Query  1443  RNNNFQTFPQAVLLLFRCATGEAWQDIMLACMPGKKCAPESEPSNSTEGETPCGS-SFAV  1501
                         N NF+T  +++++LFRC+ GE W  IM      +     S   NST   T CGS ++A
Sbjct  1690  DNINFRTVIKSMIVLFRCSFGEGWNYIMADLTVSEPYC--SSDDNST--YTDCGSETYAY  1745

Query  1502  FYFISFYMLCAFLIINLFVAVIMDNFDYLTRDW---SILGPHHLDEFKRIWAEYDPEAKG  1558
                          +S+ ++  ++ +N+FV++I+ NF Y+ R     S +    + ++   W+++D +  G
Sbjct  1746  LLLMSWNIISMYIFVNMFVSLIIGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFDTDGTG  1805

Query  1559  RIKHLDVVTLLRRIQPPLGFGKLCPHRVACKRLVSMNMPLNSD  1601
                         ++   +  ++     PL F K+   R+  K LV   M +N D
Sbjct  1806  ELELSYLPRIMHSFDGPLSF-KIWEGRLTIKSLVENYMEVNPD  1847
```

Ion transport protein [Streptococcus pneumoniae]
CJK91097.1 279 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
53.1 bits(126)	3e-05	Compositional matrix adjust.	57/267(21%)	113/267(42%)	63/267(23%)

```
Query  957   DYVFTSIFTLEIILKMTAYGAFLHKGSFCRNYFNILDLLVVSVSLISFGIQSSAINVVKI  1016
                    D +  ++F  EI  ++     ++H+ +F R+ +++ D  VV+++L+      S +  +++
Sbjct  57    DSLILAVFVAEIAARI-----YVHRAAFFRDPWSLFDFSVVAIALVPASGPFSILRALRV  111

Query  1017  LRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIVIVTTLLQFMFACIGVQLFKGKLY  1076
                    LRV+R+      +     ++ VV  +  AI  +G+I +V  L+ ++ A I   LF
Sbjct  112   LRVMRM------VTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAA---  162

Query  1077  TCSDSSKQTEAECKGNYITYKDGEVDHPIIQPRSWENSKFDFDNVLAAMMALFTVSTFEG  1136
                                                    D P      W      F ++  ++  LF V T E
Sbjct  163   -------------------------DFP-----EW------FGSLGRSVYTLFQVMTLES  186

Query  1137  WPELLYRSIDSHTEDKGPIYNYRVEISIFFIYIIIIAFFMMNIFVGFVIVTFQEQGEQE  1196
                    W   + R +        I+ Y     +FFI +I+I  F M+N+F+  ++   Q   + +
Sbjct  187   WSMGIVRPVME-------IFPYA---WVFFIPFILIATFTMLNLFIAIIVNAMQTVTDAD  236

Query  1197  YKNCELD-KNQRQCVEYAL--KARPLR  1220
                    +  +   +  R+ +E  L  + R LR
Sbjct  237   REATQASIEAAREHIETDLHDEVRALR  263
```

S protein, partial [Hepatitis B virus]
AOF42255.1 134 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
33.5 bits(75)	22	Composition-based stats.	19/41(46%)	22/41(53%)	2/41(4%)

```
Query  2012  ALAVAGLSP--LLQRSHSPASFPRPFATPPATPGSRGWPPQ  2050
             +L V G SP  L Q S SP S   P + PP  PG RG  P+
Sbjct  9     SLNVLGGSPVCLGQNSQSPTSNHSPTSCPPICPGYRGMCPR  49
```

Uncharacterised protein [Bordetella pertussis]
CFN80739.1 30 1

See 1 more title(s)

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	135	Composition-based stats.	14/28(50%)	17/28(60%)	0/28(0%)

```
Query  1826  LPRPAGYPSTVSTVEGHGPPLSPAIRVQ  1853
             +P P G  S VS   G GP LSPA+ V+
Sbjct  1     MPLPLGPSSAVSVPCGKGPRLSPAMTVR  28
```

DNA repair protein RecO [Neisseria meningitidis]
WP_025455575.1 247 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.4 bits(67)	431	Compositional matrix adjust.	21/67(31%)	33/67(49%)	13/67(19%)

```
Query  1277  LFTGLFTVEMILKLIAFKPKGYFSDPW-NVFDFLIVIGSIIDVILSETNHYF---CDAWN  1332
             LF+GL+  E++LKL A +      DP   ++D L     +++ +  E NH     C  W
Sbjct  90    LFSGLYVNELVLKLTARE------DPMPELYDAL---AKVMEAVCREANHIADLRCFEWK  140

Query  1333  TFDALIV  1339
               +AL V
Sbjct  141   LLNALGV  147
```

hypothetical protein W5M_06852 [Corynebacterium diphtheriae bv. intermedius str. NCTC 5011]
EIK56196.1 91 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	1424	Composition-based stats.	10/23(43%)	13/23(56%)	0/23(0%)

```
Query  2022  LQRSHSPASFPRPFATPPATPGS  2044
             +  SH+P   PRP A P   PG+
Sbjct  1     MSTSHTPKPGPRPGAVPGPRPGA  23
```

serine/threonine protein kinase [Clostridium tetani]
WP_052219511.1 619 1

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.3 bits(64)	1432	Composition-based stats.	14/32(44%)	19/32(59%)	2/32(6%)

```
Query  1939  TEMLSYQDDENRQLTLPEED--KRDIRQSPKR  1968
             TE  + Q+DEN  +T PEED  K D +Q   +
Sbjct  585   TEEPTDQEDENNNITTPEEDGKKEDTKQDKNK  616
```

hypothetical protein [Haemophilus influenzae]
WP_041174642.1 112 1

See 2 more title(s)

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	2520	Composition-based stats.	15/55(27%)	31/55(56%)	7/55(12%)

```
Query  654  LLLLLFLFIIIFSLLGMQLFGGKFNFDEMQTRRSTFDNFPQSLLTVFQILTGEDW  708
            + L+LFLFI + SL+G++       ++++ ++   F+       TVF+   GE++
Sbjct  3    ICLVLFLFISLSSLMGLK-------YNKLSSQLFIFNILIIYFFTVFRYDVGEEY  50
```

No matches to measles, mumps, rubella, polio or human influenza A viruses, in the first 10000 results.

E3 ubiquitin-protein ligase TRIM21 (Ro/SSA)

Slx8p [Saccharomyces cerevisiae YJM1248]
AJU44904.1 274 1

See 2 more title(s)

GenPeptGraphics Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
39.7 bits(91)	0.097	Compositional matrix adjust.	18/54(33%)	27/54(50%)	5/54(9%)

```
Query  16   CPICLDPFVEPVSIECGHSFCQECISQVGKGGGSV-----CPVCRQRFLLKNLR  64
            CPIC +P    +   CGH FC  C+ Q+     +      C +CR +  LK++R
Sbjct  206  CPICFEPPETALMTLCGHVFCCPCLFQMVNSSRTCRQFGHCALCRSKVYLKDVR  259
```

flagellar export protein FliJ [Clostridium tetani]
WP_035109535.1 145 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.6 bits(70)	21	Composition-based stats.	14/54(26%)	36/54(66%)	1/54(1%)

```
Query  139  LQVALGELRRKQELAEKLEVEIAIKRADWKKTVETQKSRIHAEFVQQKNFLVEE  192
            +++   EL++++E  EK+ + +  K+ + +KTVET + +  + F++++N L ++
Sbjct  76   IELTTEELKKREEEVEKVRISLKQKQIE-RKTVETLREKDKSAFIKEQNLLEQK  128
```

PqiA, partial [Neisseria meningitidis]
AAK08046.1 103 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	57	Composition-based stats.	10/36(28%)	19/36(52%)	0/36(0%)

```
Query  19  CLDPFVEPVSIECGHSFCQECISQVGKGGGSVCPVC  54
           C D  + P +++C    C+  + Q+ +G  + CP C
Sbjct  16  CRDEALPPHTVDCPECGCRADVPQLDRGEAAFCPRC  51
```

hypothetical protein BXA20_11850 [Corynebacterium diphtheriae]
ONF63907.1 115 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	59	Compositional matrix adjust.	14/34(41%)	19/34(55%)	4/34(11%)

```
Query  94   VHGERLHLFCEKDGKALCWV----CAQSRKHRDH  123
            +HG+RLH FC+     LC+       QS+ H DH
Sbjct  24   LHGDRLHSFCDYRHILLCYSRSLPTPQSQPHTDH  57
```

IclR family transcriptional regulator [Bordetella pertussis]
WP_023852623.1 256 1

See 554 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.0 bits(66)	106	Compositional matrix adjust.	23/76(30%)	36/76(47%)	8/76(10%)

```
Query  96   GERLHLFCEKDGKALCWVCAQSRKHRDHAMVPLEEAAQEYQEKLQVALGELRRKQELAEK  155
            G R   +    GKAL  +  Q+  + DH       A + + E   V+L  L  KQELA+
Sbjct  128  GGRAPAYAVATGKAL--LACQTADYLDH----YGAAIKRHTEDTHVSL--LALKQELADV  179

Query  156  LEVEIAIKRADWKKTV  171
              +  AI R +W++ +
Sbjct  180  NRIGYAINRGEWRQGI  195
```

diphosphonucleoside choline transferase [Haemophilus influenzae]
ADQ55242.1 265 1

See 3 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.6 bits(52)	6481	Compositional matrix adjust.	12/52(23%)	23/52(44%)	9/52(17%)

```
Query  6   RLTMMWEEVTCPICLDPFVEPVSIECGHSFCQECISQVGKGGGSVCPVCRQR  57
           +LT+  +++ C   LD F         H+ C++       GGG++    R +
Sbjct  3   KLTLREQQLVCLDILDYF---------HALCEKYQIHYSLGGGTLIGAIRHK  45
```

No matches to measles, mumps, rubella, polio, hepatitis A/B or human influenza A viruses, in the first 10000 results.

Potassium voltage-gated channel subfamily KQT member 1 (K$_V$LQT1 α)

ion transport protein [Streptococcus pneumoniae]
CJL53225.1 283 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
62.4 bits(150)	8e-11	Compositional matrix adjust.	64/256(25%)	111/256(43%)	46/256(17%)

```
Query  129  VFLIVLVCLIFSVLSTIEQYAALATGTLFWMEIVLVVFFGTEYVVRLWSAGCRSKYV-GL  187
            +F  ++V ++ S+ S  E++  L T     +E      F  EYV+R+++     KY+
Sbjct  38   IFASLVVVMLDSIASFNERHGQLLTN----LEWGFTAIFAVEYVLRIYTHPEPRKYILSF  93

Query  188  WGRLRFARKPISIIDLIVVVASMVVLCVGSKGQVFATSAIRGIRFLQILRM---------  238
            +G          ++DL  V+ + + L       +     IR +R  ++L++
Sbjct  94   YG----------MVDLFSVLPAFIALLFPDAQYLLVVRVIRMLRIFRVLKLAPYLSQANF  143

Query  239  LHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGS  298
            L V  QG   ++   +VF+     +TTL I +  L++            V E     F S
Sbjct  144  LLVALQGSRQKI---IVFLLS---VTTLIIVYGTLMY------------VIEGPSNGFTS  185

Query  299  YADALWWGVVTVTTIGYGDKVPQTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQK  358
               +++W VVT+TT+G+GD VP T +GK +A+   +   S  A+P GI    F  ++
Sbjct  186  IPISIYWAVVTLTTVGFGDIVPLTPLGKALATVVMITGYSIIAVPTGI----FTAELANA  241

Query  359  QRQKHFNRQIPAAASL  374
             RQ       P    L
Sbjct  242  MRQDSLRHNCPTCDKL  257
```

potassium channel protein [Bordetella pertussis]
CFW09189.1 319 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps

38.1 bits(87) 0.006 Compositional matrix adjust. 25/87(29%) 41/87(47%) 7/87(8%)

```
Query  300  ADALWWGVVTVTTIGYGDKVPQTWVGKTIASCFSVFAISFFALPAGILGS---GFALKVQ  356
            A A ++ +V+++T+GYGD  PQT   +  A+   +  I+ FA     +     G  LK
Sbjct  96   ATAFYFSIVSMSTVGYGDITPQTTAARLFAASIIILGITVFATSISAIAGPVIGGNLKRL  155

Query  357  QKQRQKHFNRQ----IPAAASLIQTAW  379
             + R  H  R+    I  A  L Q+ +
Sbjct  156  VRGRISHAMRKHHIIIAGATPLAQSVY  182
```

hypothetical protein [Corynebacterium diphtheriae]
WP_072588026.1 162 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	20	Compositional matrix adjust.	25/84(30%)	35/84(41%)	12/84(14%)

```
Query  249  RLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEF--GSYADALWWG  306
            R+LG     HR EL+T    G          VY     A  +  R+ F   S A  +WW
Sbjct  32   RILG-----HRVELVTDASRGPEQDRHHREVVY-----AWLQGLRIPFLIASMATYMWWH  81

Query  307  VVTVTTIGYGDKVPQTWVGKTIAS  330
             V V+ I +   +P  W+   IA+
Sbjct  82   NVVVSVILFVICIPLPWIAVVIAN  105
```

30S ribosomal protein S11 [Clostridium tetani]
WP_011100698.1 132 1

See 9 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
23.5 bits(49)	151	Compositional matrix adjust.	7/14(50%)	10/14(71%)	0/14(0%)

```
Query  440  VPHITCDPPEERRL  453
            +PH  C PP+ RR+
Sbjct  119  IPHNGCRPPKRRRV  132
```

helix-hairpin-helix motif family protein [Neisseria meningitidis NM045]
EQD03286.1 69 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	3.0	Composition-based stats.	11/16(69%)	11/16(68%)	0/16(0%)

```
Query  57  GAPGPAPPASPAAPAA  72
           GAP P  PA PA PAA
Sbjct  52  GAPAPKGPAKPAIPAA  67
```

DNA internalization-related competence protein ComEC/Rec2 [Haemophilus influenzae]
WP_042603513.1 788 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	12	Compositional matrix adjust.	17/45(38%)	18/45(40%)	3/45(6%)

```
Query  370  AAASLIQTAWRCYAAENPDSSTWKIYIRKAPRSHTLLSPSPKPKK  414
            A   +   WR Y      SSTWKI   K PR  TL    P  K
Sbjct  464  CAGIFMLIIWRIYREPEASSSTWKI---KRPRFFTLNLSKPLLKN  505
```

non-structural polyprotein p200 [Rubella virus]
AEN94545.1 2116 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
20.4 bits(41)	2684	Compositional matrix adjust.	19/61(31%)	24/61(39%)	3/61(4%)

```
Query  65   ASPAAPAAPPVASD-LGPRPPVSLDPRVSIYSTRRPVLARTHVQGRVYNFLERPTGWKCF  123
            A  A  A   VA D  GP  P   DP   I  +        H+  RV + ++ P G K
Sbjct  779  ADRARDAEQEVACDPSGPAAPTRADPNSDIVESYARAAGPVHL--RVRDIMDPPPGCKVV  836

Query  124  V  124
            V
Sbjct  837  V  837
```

surface antigen, partial [Hepatitis B virus]
AAR87403.1 101 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
24.3 bits(51)	58	Compositional matrix adjust.	13/22(59%)	16/22(72%)	2/22(9%)

```
Query  119  GWKCFVYHFAVFL-IVLVCLIF  139
            GW C +  F +FL I+LVCLIF
Sbjct  14   GWMC-LRRFIIFLFILLVCLIF  34
```

No matches to measles, mumps, polio, hepatitis A or human influenza A viruses, in the first 10000 results.

Sodium channel protein type 5 subunit alpha (SCN5A)

Ion transport protein [Streptococcus pneumoniae]
CJK91097.1 279 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
69.7 bits(169)	1e-10	Compositional matrix adjust.	67/279(24%)	115/279(41%)	63/279(22%)

```
Query  1195  RKTCYHIVEHSWFETFIIFMILLSSGALAFE-DIYLEERKTIKVLLEYADKMFTYVFVLE  1253
             R     +E   F+  I+ +I++++  L  +    L  R    ++L   D +   VFV E
Sbjct  10    RSRLGQFIERPAFQRGILLLIVINAAILGMQTSAALVARWGEALVL--LDSLILAVFVAE  67

Query  1254  MLLKWVAYGFKKYFTNAWCWLDFLIVDVSLVSLVANTLGFAEMGPIKSLRTLRALRPLRA  1313
             +  +   +    +F + W   DF +V ++LV          GP   LR LR LR +R
Sbjct  68    IAARIYVHR-AAFFRDPWSLFDFSVVAIALVP---------ASGPFSILRALRVLRVMRM  117

Query  1314  LSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFGRCINQTEGDLPL  1373
             ++    MR VV AL+ AIP + ++ +V  + + + +++   LFA  F
Sbjct  118   VTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAADFPE----------  166

Query  1374  NYTIVNNKSQCESLNLTGELYWTKVKVNFDNVGAGYLALLQVATFKGW-MDIMYAAVDSR  1432
                                                W      F ++G     L QV T + W M I+
Sbjct  167   ----------------------W------FGSLGRSVYTLFQVMTLESWSMGIV-------  192

Query  1433  GYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIID  1471
                          +P  E   Y +++F+ FI+  +F  LNLFI +I++
Sbjct  193   ----RPVMEIFPYAWVFFIPFILIATFTMLNLFIAIIVN  227
```

Cch1p [Saccharomyces cerevisiae YJM270]
AJR78792.1 2039 2

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
70.9 bits(172)	3e-10	Compositional matrix adjust.	75/349(21%)	140/349(40%)	65/349(18%)

```
Query  115   SPFHPIRRAAVKILVHSLFNMLIMCTILTNCVFMAQHDPPPW--TKYVEYTFTAIYTFES  172
              S FH I R     +      +LI+C+     ++   H    W  +  ++  F   ++ E
Sbjct  1198  SYFHHIERDVFVFIFALATILLIVCSCYVTPLYRMHHKMGTWNWSSALDCAFIGAFSIEF  1257

Query  173   LVKILARGFCLHAFTFLRDPWNWLDFSVIIMAYTTEFVDLGNVSAL-RTFRVLRALKTIS  231
                      +VK +A GF      +LR+PWN++DF V+I  +      L N   L R F+ L AL+ +
Sbjct  1258  IVKTVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALR  1317

Query  232   VI----SGLKTIVGALIQSVKKLADVMVLTVFCLSVFALIGLQLFMGNLRHKCVRNFTAL  287
                      +   + +T   + K+ +  ++++  L  F + GL +F G L       T
Sbjct  1318  CLTISNTARQTFNLVMFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRLG-------TCN  1370

Query  288   NGTNGSVEADGLVWESLDLYLSDPENYLLKNGTSDVLLCGNSSDAGTCPEGYRCLKAGEN  347
                      +G+ G  +                      C N            +  +
Sbjct  1371  DGSLGRAD----------------------------CYNEYSNSVFQWDIMSPRVYQQ  1400

Query  348   PDHGYTSFDSFAWAFLALFRLMTQDCWERLYQQTLRSAG----------KIYMIFFMLVI  397
                      P   Y   DSFA AF +L+++++ + W  L +  + S+G            +F +L I
Sbjct  1401  P---YLHLDSFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVLFI  1457
```

```
Query  398   FLGSFYLVNLILAVVAMAYEEQNQATIAETEE---KEKRFQEAMEMLKK  443
                    FL  +++NL ++ +     NQA   +    +EK + E+ ++L +
Sbjct  1458  FLSMVFILNLFVSFIV-----NNQARTTGSAYFTIEEKAWLESQKLLSQ  1501
```

dihydroorotase, partial [Bordetella pertussis]
WP_019249695.1 337 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.6 bits(70)	193	Composition-based stats.	28/92(30%)	36/92(39%)	23/92(25%)

```
Query  569  RTSAQGQPSPGTSAPGHALHGKKNSTVDCNGVVSLLGAGDPEATSPGSHLLRPVMLEH--  626
            R +A GQ   G  A  H         +D  G+  L G  D  A   G+ L  P+  E
Sbjct  32   RIAAIGQAPAGFQAQQH---------IDARGLAVLPGLVDLSARVHGAGL-APLACEMQA  81

Query  627  -----------PPDTTTPSEEPGGPQMLTSQA  647
                       PPDT  P +EPG  +ML  +A
Sbjct  82   ALAGGVTRLVVPPDTDPPLDEPGRVEMLRHRA  113
```

hypothetical protein KY52_09675 [Clostridium tetani]
KGI37804.1 553 1

See 3 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
35.8 bits(81)	12	Composition-based stats.	48/193(25%)	87/193(45%)	33/193(17%)

```
Query  1432  RGYEEQPQWEYNLYMYIYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGQDIFMTEEQ  1491
             R Y+ +     +++ Y+Y +I          + LF   +I N+           D+ +T
Sbjct  282   RSYKIKKNIVRDIFFYVYNIIISFNIILVFVILFFASVIKNWPY--------DLSIT---  330

Query  1492  KKYYNAMKKLGSKKPQKPIPRPLNKYQGFIFDIVTKQAFDVTIMFLICLNMVTMMVETDD  1551
               KYYN +K +G+           LN Y+  IF      AF   ++  I + +   +VE
Sbjct  331   LKYYN-VKSVGTSL--------LNVYKNTIF-----VAFTTALIGTIVVFITAYIVERYK  376

Query  1552  QSPEKINILAKINLLFVAIFTGECIVKLAALRHYYFTNSWNIFDFVVVILSIVGTVLSDI  1611
             +  +  NIL  I  L ++I     ++ L+ +   +F  SWN+F+F+     I+  +L++I
Sbjct  377   EFSKIRNILYIIASLPLSI--SGMVIGLSYI--LFFNKSWNVFNFLYGTFFIL--ILANI  430

Query  1612  IQKYFFSPTLFRV  1624
             I  +FFS   F +
Sbjct  431   I--HFFSVPFFTI  441
```

hypothetical protein, partial [Corynebacterium diphtheriae]
WP_071575429.1 144 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	4634	Composition-based stats.	9/17(53%)	13/17(76%)	0/17(0%)

```
Query  1493  KYYNAMKKLGSKKPQKP  1509
             KYYN+ +  G KKP++P
Sbjct  123   KYYNSDQSSGPKKPERP  139
```

hypothetical protein, partial [Haemophilus influenzae]
WP_005655715.1 133 1

See 7 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.0 bits(71)	54	Composition-based stats.	20/70(29%)	34/70(48%)	5/70(7%)

```
Query  1212  IFMILLSSGALAFEDIYLEERKTIKVLLEYADKM-----FTYVFVLEMLLKWVAYGFKKY  1266
             +++  +S  +L F  IYLE R  + +LL+YAD +      +Y+  + + L W+    K
Sbjct  18    LYLTFVSVTSLFFISIYLENRPLLSLLLDYADNIDRLSSLSYITSVLLSLFWIYKAHKNI  77

Query  1267  FTNAWCWLDF  1276
                    LDF
Sbjct  78    EQKGIKNLDF  87
```

Uncharacterised protein [Neisseria meningitidis]
CWS47831.1 109 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.1 bits(61)	980	Compositional matrix adjust.	13/33(39%)	17/33(51%)	0/33(0%)

```
Query  978   WDFCCGLLRQRPQKPAALAAQGQLPSCIATPYS  1010
              W     LL Q+  +PA LAA  +LP C+    S
Sbjct  45    WSAASFLLWQKKPQPAYLAAAARLPDCLLVAVS  77
```

surface antigen, partial [Hepatitis B virus]
AGZ62121.1 148 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	2332	Composition-based stats.	25/97(26%)	32/97(32%)	5/97(5%)

```
Query  564  PWPLRRTSAQGQPSPGTSAPGHALHGKKNSTVDCNGVVSLLGAGDPEATSPGSHLLRPVM  623
            PWP       G   PG + P   L G    +    G++  L A  P A++      +P
Sbjct  50   PWPDANKVGAGAFGPGVTPPHGGLLG---WSPQAQGILQTLPANPPPASTNRQSGRQPTP  106

Query  624  LEHPPDTTTPSEEPGGPQML--TSQAPCVDGFEEPGA  658
            L  P   T P            T Q P V G   P
Sbjct  107  LSPPLRDTHPQAMQWNSTTFQQTLQDPXVRGLYFPAG  143
```

No matches to measles, mumps, rubella, hepatitis A, human influenza A, human papilloma or polio viruses, in the first 10000 results.

Potassium voltage-gated channel subfamily H member 2 (KCNH2)

Phototropin homolog [Streptococcus pneumoniae]
CON50322.1 261 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
55.1 bits(131)	2e-06	Composition-based stats.	30/105(29%)	52/105(49%)	2/105(1%)

```
Query  15   LDTIIRKFEGQSRKFIIANARVENCAVIYCNDGFCELCGYSRAEVMQRPCTCDFLHGPRT  74
            L+ I +  +      +I +  +E+  ++Y N GF ++ GY   E++ +   C FL G  T
Sbjct  13   LEVIKKALDHVRVGVVITDPALEDNPIVYVNQGFVQMTGYETEEILGK--NCRFLQGKHT  70

Query  75   QRRAAAQIAQALLGAEERKVEIAFYRKDGSCFLCLVDVVPVKNED  119
                    I  AL   E   V+I  Y+KDG+ F   +++ P++ ED
Sbjct  71   DPAEVYNIRTALQNKEPVTVQIQNYKKDGTMFWNELNIDPMEIED  115
```

transcriptional regulator Crp [Haemophilus influenzae]
WP_050846696.1 224 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
44.3 bits(103)	0.006	Compositional matrix adjust.	25/90(28%)	44/90(48%)	6/90(6%)

```
Query  764  PPGDTLVHAGDLLTALYFISRGSIEILRGD-----VVVAILGKNDIFGEPLNLYARPGKS  818
            P   TL+HAG+  T LY++ +GS+ +   D     +++  LG    FGE   L+    K
Sbjct  39   PAKSTLIHAGEDATTLYYVIKGSVMVSSKDDEGKEMILTYLGAGQFFGEA-GLFDEGSKR  97

Query  819  NGDVRALTYCDLHKIHRDDLLEVLDMYPEF  848
            +  V+  T C++ +I      +++   PE
Sbjct  98   SAWVKTKTTCEIAEISYKKYRQLIQANPEI  127
```

potassium channel protein [Bordetella pertussis]
CFU09599.1 364 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
44.7 bits(104)	0.009	Compositional matrix adjust.	24/89(27%)	51/89(57%)	8/89(8%)

```
Query  613  TALYFTFSSLTSVGFGNVSPNTNSEKIFSICVMLIGSLMYASIFGNVSAIIQRLYSGTAR  672
            TA YF+  S+++VG+G+++P T + ++F+  ++++G  ++A+   ++SAI   +  G  +
Sbjct  142  TAFYFSIVSMSTVGYGDITPQTTAARLFAASIIILGITVFAT---SISAIAGPVIGGNLK  198
```

```
Query  673  YHTQMLRVREFIRFHQI----PNPLRQRL  697
              +  R+   +R H I      PL Q +
Sbjct  199  RLVRG-RISHAMRKHHIIIAGATPLAQSV  226
```

hypothetical protein [Clostridium tetani]
WP_035125131.1 88 1

See 5 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.6 bits(65)	95	Composition-based stats.	9/19(47%)	14/19(73%)	0/19(0%)

```
Query  695  QRLEEYFQHAWSYTNGIDM  713
            +++ EY  HAW Y NG++M
Sbjct  70   KQINEYVDHAWIYENGVEM  88
```

NAD-binding protein of Kef-type K+ transporter [Corynebacterium diphtheriae]
WP_004567149.1 362 1

See 90 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
37.4 bits(85)	1.9	Compositional matrix adjust.	14/43(33%)	29/43(67%)	0/43(0%)

```
Query  603  GGPSIKDKYVTALYFTFSSLTSVGFGNVSPNTNSEKIFSICVM  645
            GG S    ++ ALY++  SL++ G+G+++P T S ++ +I ++
Sbjct  69   GGYSEHLTFIDALYYSAVSLSTTGYGDITPITQSARLLNIIII  111
```

Sod1p [Saccharomyces cerevisiae YJM1304]
AJV39167.1 154 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
33.5 bits(75)	13	Composition-based stats.	23/80(29%)	38/80(47%)	9/80(11%)

```
Query  739  HCKPFRGATKGCLRALAM--KFKTTHAPPGDTLVHAGDL---LTALYFISRGSIEILRGD  793
            H   F  AT GC+ A      FK TH  P D + H GD+    T    +++GS +    D
Sbjct  47   HIHEFGDATNGCVSAGPHFNPFKKTHGAPTDEVRHVGDMGNVKTDENGVAKGSFK----D  102

Query  794  VVVAILGKNDIFGEPLNLYA  813
             ++ ++G   + G  + ++A
Sbjct  103  SLIKLIGPTSVVGRSVVIHA  122
```

glycosyltransferase 25 family protein, partial [Neisseria meningitidis 69096]
ELL13802.1 44 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	302	Compositional matrix adjust.	16/40(40%)	18/40(45%)	5/40(12%)

```
Query  218  MDNHVAGLGPAEERRALVGPGSPPRSAPGQ-----LPSPR  252
            M NHV  L  A ERRA +      R  P Q     +PS R
Sbjct  1    MQNHVISLASAAERRAHIAATFGARGIPFQFFDALMPSER  40
```

No matches to measles, mumps, rubella, polio, hepatitis A/B, human influenza A or human papilloma viruses, in the first 10000 results.

Potassium voltage-gated channel subfamily A member 4 (KCNA4)

ion transport protein [Streptococcus pneumoniae]
CJL53225.1 283 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
91.7 bits(226)	9e-19	Compositional matrix adjust.	53/174(30%)	95/174(54%)	15/174(8%)

```
Query  382  FSFEFVVRCFACPSQALFFKNIMNIIDIVSILPYFITLGTDLAQQQGGGNGQQQQAMSFA  441
            F+ E+V+R +  P    +  +   ++D+ S+LP FI L    AQ
Sbjct  72   FAVEYVLRIYTHPEPRKYILSFYGMVDLFSVLPAFIALLFPDAQY-------------LL  118

Query  442  ILRIIRLVRVFRIFKLSRHSKGLQILGHTLRASMRELGLLIFFLFIGVILFSSAVYFAEA  501
            ++R+IR++R+FR+ KL+ +      L   L+ S +++ + +  +   +I++ + +Y  E
Sbjct  119  VVRVIRMLRIFRVLKLAPYLSQANFLLVALQGSRQKIIVFLLSVTTLIIVYGTLMYVIEG  178

Query  502  DEPTTHFQSIPDAFWWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAGVLTIALP  555
               P+  F SIP + +WAVVT+TTVG+GD+ P+T  GK + ++  I G   IA+P
Sbjct  179  --PSNGFTSIPISIYWAVVTLTTVGFGDIVPLTPLGKALATVVMITGYSIIAVP  230
```

potassium channel protein [Bordetella pertussis]
CFW09189.1 319 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
39.3 bits(90)	0.21	Compositional matrix adjust.	37/141(26%)	65/141(46%)	20/141(14%)

```
Query  429  GGNGQQQQAMSFAILRIIRLVRVFRIFKLSRHSKGLQILGHTLRASMRELGLLIFFLFIG  488
            G +G     +++  + I  LV  +R F  +  + G      +L A +    LLI+ +F
Sbjct  28   GWDGGHGLLLAYTGVLIAALVCFWRRFDRASLAAG------SLFAVISITSLLIYAVF--  79

Query  489  VILFSSAVYFAEADEPTTHFQSIPDAFWWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAG  548
              L+  A +  + + P T       AF++++V+M+TVGYGD+ P T   ++  +   I G
Sbjct  80   GTLYLGAEFSPKVESPAT-------AFYFSIVSMSTVGYGDITPQTTAARLFAASIIILG  132
```

```
Query  549  VLTIALPV-----PVIVSNFN  564
              +   A  +     PVI  N
Sbjct  133  ITVFATSISAIAGPVIGGNLK  153
```

NAD-binding protein of Kef-type K+ transporter [Corynebacterium diphtheriae]
WP_004567149.1 362 1

See 90 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
37.4 bits(85)	1.00	Compositional matrix adjust.	21/81(26%)	43/81(53%)	2/81(2%)

```
Query  464  LQILGHTLRASMRELGLLIFFLFIGVILFSSAVYFAEADEPTTHFQSIPDAFWWAVVTMT  523
            ++I G+ L + +R +     +    +I+ +  VY  E    + H   I DA +++ V+++
Sbjct  32   IRIPGNPLVSPIRLIARRFGYALALIIIVALVVYLDEGGY-SEHLTFI-DALYYSAVSLS  89

Query  524  TVGYGDMKPITVGGKIVGSLC  544
            T GYGD+ PIT   +++  +
Sbjct  90   TTGYGDITPITQSARLLNIII  110
```

hypothetical protein H760_YJM456O00189 [Saccharomyces cerevisiae YJM456]
AJT77342.1 715 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.3 bits(59)	1490	Compositional matrix adjust.	15/53(28%)	27/53(50%)	5/53(9%)

```
Query  92   KKKAHYRQSSFPHCSDLMPSGSE-----EKILRELSEEEEDEEEEEEEEEGR  139
            K+ AHY Q+  PHCS+     S+     E I ++L   +E+  + ++   E +
Sbjct  588  KEMAHYEQTYLPHCSEAYGLTSKVLEFGENIWKDLPGTDENNLQSKKNSPEKK  640
```

neuraminidase [Influenza A virus (A/swine/Iowa/A01203491/2012(H1N1))]
AFN66863.1 469 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.6 bits(57)	2736	Compositional matrix adjust.	13/45(29%)	27/45(60%)	1/45(2%)

```
Query  540  VGSLCAIAGVLTIALPVPVIVSNFNYFYHRETENEEQTQLTQNAV  584
            +G++C IAG++++ L +  IVS +   +  +T  E  T++   +V
Sbjct  10   IGTVCMIAGIISLLLQIGNIVSLW-ISHSIQTGWENHTEMCNQSV  53
```

hypothetical protein [Haemophilus influenzae]
WP_050845276.1 458 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.2 bits(56)	3554	Compositional matrix adjust.	12/33(36%)	18/33(54%)	1/33(3%)

```
Query  511  IPDAFWWAVVTMTTVGYGDMKPITVGGKIVGSL  543
            I D  WWA     T+ +G +KP T+ G I  ++
Sbjct  7    IYDNTWWAKAHQFTITHGGLKP-TLRGTIKNTM  38
```

DNA damage-inducible protein DnaD [Neisseria meningitidis]
WP_049344716.1 283 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
30.0 bits(66)	158	Compositional matrix adjust.	21/66(32%)	27/66(40%)	17/66(25%)

```
Query  498  FAEADEPTTHFQSIPDAFWWAVVTMTTVGYGDMKPITVGGKIVGSLCAIAGVLTIALPVP  557
            FA+ADE T         FW+A      +GY DM+ I        S+C         L +P
Sbjct  26   FAQADENT---------FWYASDLAMMLGYNDMQAILKAINRAHSVC-------FQLDIP  69

Query  558  VIVSNF  563
             I  NF
Sbjct  70   -ITENF  74
```

No matches to C. tetani, measles, mumps, rubella, polio, hepatitis A/B or human papilloma viruses, in the first 10000 results.

Voltage-dependent L-type calcium channel subunit alpha-1S (CACNA1S)

Cch1p [Saccharomyces cerevisiae YJM1385]
AJS26017.1 2039 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
172 bits(437)	3e-41	Compositional matrix adjust.	228/1043(22%)	427/1043(40%)	152/1043(14%)

```
Query  526  VLRCIRLLRIFKITKYWTSLSNLVASLLNSIRSIASLLLLLFLFIVIFALLGMQLFGGRY  585
                + R  R++  FK+TK      L   +L++   I +L    F F  + A++    F G
Sbjct  871  ISRFYRVIISFKLTK------KLWKQILSNGVMIWNLSSFYFFFTFLVAIIMAVYFEGVI  924

Query  586  DFEDTEVRRSNFDNFPQALISVFQVLTGEDWTSMMYNGIMAYGGPSYPGMLVC-IYFIIL  644
                     E+   +     + P + +S+F + + E+WT ++Y   +    P+     C ++FII
Sbjct  925  PPEEMADQPFGMYSLPNSFLSLFIIGSTENWTDILY--ALQKHSPNISSAFFCSVFFIIW  982

Query  645  FVCGNYILLNVFLAIAVDNLAEAESLTSAQKAKAEEKKRRKMSKGL----PDKSEE--EK  698
                    F+  N ++LN+F+A+A+        ++ + + K EEK+ +++   L    P K +E
Sbjct  983  FLLSNSVILNIFIAL----------ISESMEVKEEEKRPQQIKHYLKFVYPQKIQEYTHA  1032
```

```
Query  699   STMAKKLEQKPKGEGIPTTAKLK--------IDEFESNVNEVKDPY---PSAD-FPGDDE  746
                    S +A+  ++   G     T   K       I     N+ E+ D +   PS + F  D
Sbjct  1033  SLVARIRKKFFGGHRNEDTRDFKQFLMRGTAIMNIAQNMGELADEFKEPPSENLFKKDLS  1092

Query  747   EDEPEIPLSPRPRPLAE----------------------LQLKE---------KAVPIP  774
                    +    +P   R R  A                    L+L E         K  P+
Sbjct  1093  KLTIGVPSLKRLRMFANNPFYKNSDVVFTETNDINGRTYILELNEYEDEKLDYLKKYPLF  1152

Query  775   EASSFFIFSPTNKIRVLCHRIV----------------NATWFTN------------FILL  807
                       S +F FSP ++ R  C R+V              ++T   N           F+ +
Sbjct  1153  NYSYYF-FSPQHRFRRFCQRLVPPSTGKRTDGSRFFEDSTDLYNKRSYFHHIERDVFVFI  1211

Query  808   FILLSSAALAAEDPIRADSMRNQIL------KHFDIGFTSVFTVEIVLKMTTYGAFLHKG  861
                    F L +   +     +   +        D  F   F++E ++K    G
Sbjct  1212  FALATILLIVCSCYVTPLYRMHHKMGTWNWSSALDCAFIGAFSIEFIVKTVADGFIYSPN  1271

Query  862   SFCRNYFNMLDLLVVA---VSLISMGLESSAIS-VVKILRVLRVLRPLRAINRAKGLKHV  917
                    ++ RN +N +D  V+    ++LI+    +  +S + K L  LR LR L   N A+   ++
Sbjct  1272  AYLRNPWNFIDFCVLISMWINLIAYLKNNGNLSRIFKGLTALRALRCLTISNTARQTFNL  1331

Query  918   VQCMFVAISTIGNIVLVTTLLQFMFACIGVQLFKGKFFRCTDLSKMTEEECRGYYYVYKD  977
                    V  MF  ++ I   L++  L F F   G+ +FKG+   C D S +   +C   Y  Y +
Sbjct  1332  V--MFDGLNKIFEAGLISLSLLFPFTVWGLSIFKGRLGTCNDGS-LGRADC---YNEYSN  1385

Query  978   GDPMQIELRHREWVHSDFHFDNVLSAMMSLFTVSTFEGWPQLLYKAIDSNAEDVGPIYNN  1037
                              +  R +    H D+  SA  SL+ + + EGW  LL   ++S+
Sbjct  1386  SVFQWDIMSPRVYQQPYLHLDSFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMG  1445

Query  1038  RVEMAIFFIIYIILIAFFMMNIFVGFVIVTFQEQGETEYKNCELD---KNQRQCVQYALK  1094
                           A+F +++  L   F++N+FV F++       + Y   E     ++Q+   Q   K
Sbjct  1446  SAGNALFLVLFNFLSMVFILNLFVSFIVNNQARTTGSAYFTIEEKAWLESQKLLSQAKPK  1505

Query  1095  ARPLRCYIPK-NPYQYQVWYIVTSSYFEYLMFALIMLNTICLGMQHYNQSEQMNHISDIL  1153
                    A P    + +   + YQ+     + Y+   +  ++ L+ I L  + YN    + +   +
Sbjct  1506  AIPNLIELSRVRQFFYQLAVEKKNFYYASFLQVVLYLHIIMLLSRSYNPGNLIGY-QGVY  1564

Query  1154  NVAFTIIFTLEMILKLMAFKARGYFGDPWNVFDF-LIVIGSIIDVILSEIDTFLASSGGL  1212
                      +  T +F ++  L +     R YF   WN     +I+I  I++ +   +    AS
Sbjct  1565  FMFSTSVFLIQEALHMCGEGPRLYFRQKWNSIRLSIIIIAFIMNAVAFHVP---ASHYWF  1621

Query  1213  YCLGGGCGNVDPDESARISSAFFRLFRVMRLIKLLSRAEGVRTLLWTFIKSFQALPYVAL  1272
                    + + G                F ++  + ++ + + +  LL T + S   +  +
Sbjct  1622  HNIKG----------------------FFLLVIFLFIIPQNDTLTELLETAMASLPPILSLTY  1662

Query  1273  LIVMLFFIYAVIGMQMFGKIALVDGTQINRNNNFQTFPQAVLLLFRCATGEAWQEILLAC  1332
                           +LF +YA+   Q+FG   L  G+    N NF+T  +++++LFRC+ GE W  I+
Sbjct  1663  TWGVLFLVYAIALNQIFGLTRL--GSNTTDNINFRTVIKSMIVLFRCSFGEGWNYIMADL  1720

Query  1333  SYGKLCDPESDYAPGEEYT-CGT-NFAYYYFISFYMLCAFLVINLFVAVIMDNFDYLTRD  1390
                    +   + +P        YT CG+  +AY   +S+ ++  ++ +N+FV++I+ NF Y+ R
Sbjct  1721  T---VSEPYCSSDDNSTYTDCGSETYAYLLLMSWNIISMYIFVNMFVSLIIGNFSYVYRS  1777

Query  1391  W---SILGPHHLDEFKAIWAEYDPEAKGRIKHLDVVTLLRRIQPPLGFGKFCPHRVACKR  1447
                           S +    + ++   W+++D +  G ++   +  ++    PL F K    R+  K
Sbjct  1778  GGSRSGINRSEIKKYIEAWSKFDTDGTGELELSYLPRIMHSFDGPLSF-KIWEGRLTIKS  1836

Query  1448  LVGMNMPLNSDGTVTFNATLFAL  1470
                    LV   M +N D       L  L
Sbjct  1837  LVENYMEVNPDDPYDVKIDLIGL  1859
```

Ion transport protein [Streptococcus pneumoniae]
CJK91097.1 279 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
62.8 bits(151)	1e-08	Compositional matrix adjust.	57/270(21%)	118/270(43%)	59/270(21%)

```
Query  1120  FEYLMFALIMLNTICLGMQHYNQ-SEQMNHISDILNVAFTIIFTLEMILKLMAFKARGYF  1178
              F+  +  LI++N   LGMQ     +     +L+    +F  E+  ++   +A  +F
Sbjct  22    FQRGILLLIVINAAILGMQTSAALVARWGEALVLLDSLILAVFVAEIAARIYVHRA-AFF  80

Query  1179  GDPWNVFDFLIVIGSIIDVILSEIDTFLASSGGLYCLGGGCGNVDPDESARISSAFFRLF  1238
                       DPW++FDF +V  +++          +SG    L                R
Sbjct  81    RDPWSLFDFSVVAIALVP-----------ASGPFSIL--------------------RAL  109

Query  1239  RVMRLIKLLSRAEGVRTLLWTFIKSFQALPYVALLIVMLFFIYAVIGMQMFGKIALVDGT  1298
                       RV+R++++++   +R ++   + +   L  +A+++ ++F++ AVI   +F
Sbjct  110   RVLRVMRMVTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAA-------  162

Query  1299  QINRNNNFQTFPQAVLLLFRCATGEAWQEILLACSYGKLCDPESDYAPGEEYTCGTNFAY  1358
                         +   F +  ++V  LF+  T E+W      S G +  P  +  P       +A+
Sbjct  163   --DFPEWFGSLGRSVYTLFQVMTLESW-------SMG-IVRPVMEIFP---------YAW  203

Query  1359  YYFISFYMLCAFLVINLFVAVIMDNFDYLT  1388
                         +FI F ++  F ++NLF+A+I++    +T
Sbjct  204   VFFIPFILIATFTMLNLFIAIIVNAMQTVT  233
```

X protein [Hepatitis B virus]
ACM40559.1 154 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.0 bits(71)	63	Composition-based stats.	25/75(33%)	35/75(46%)	9/75(12%)

```
Query  1699  TRGRALGQPCRVLGPHSKPCVEMLKGL-LTQRAMPRGQAPPA-PC-----QCPRVESSMP  1751
             +RGR L   P    L P S PCV     G   L+ R +P       A PC         R+E+++
Sbjct  25    SRGRPLPGPLGTLSPASPPCVPTDHGAHLSLRGLPVCAFSSAGPCALRFTSARRMETTVN  84

Query  1752  EDRKSSTPGSLHEET  1766
             + R  + P  LH+ T
Sbjct  85    DHR--NLPKVLHKRT  97
```

multicopper oxidase [Corynebacterium diphtheriae PW8]
AEX68733.1 397 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
32.3 bits(72)	137	Composition-based stats.	15/35(43%)	18/35(51%)	5/35(14%)

```
Query  1734  GQAPPAPCQCPRV-----ESSMPEDRKSSTPGSLH  1763
             GQAPP  C+ PRV       S +PE  +  TP   H
Sbjct  347   GQAPPPRCRLPRVVVHRTASVLPEASRPCTPARGH  381
```

ABC transporter permease, partial [Clostridium tetani]
KHO33579.1 71 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5621	Composition-based stats.	7/22(32%)	16/22(72%)	0/22(0%)

```
Query  1366  MLCAFLVINLFVAVIMDNFDYL  1387
             ++CA +V++L +  + DNF ++
Sbjct  37    IICALIVVHLLIPFVKDNFTHI  58
```

hypothetical protein, partial [Bordetella pertussis]
WP_023997416.1 94 1

See 2 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	7523	Composition-based stats.	8/18(44%)	13/18(72%)	0/18(0%)

```
Query  977   DGDPMQIELRHREWVHSD  994
             DGD +++ ++ R WVH D
Sbjct  54    DGDALRLAVKLRLWVHVD  71
```

hypothetical protein [Haemophilus influenzae]
WP_085024506.1 495 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	2998	Composition-based stats.	13/53(25%)	33/53(62%)	5/53(9%)

```
Query  664  LAEAESLTSAQKAKAEEKKRR-----KMSKGLPDKSEEEKSTMAKKLEQKPKG  711
            +A+A++     Q+AKAE+ KR+      K+++   ++++ ++  +A++ E+  K
Sbjct  1    MAQAQAEARRQQAKAEQVKRQQAEAEKVARQKAEEAKRQQEALARQQEEARKA  53
```

peptidase [Neisseria meningitidis]
WP_049328404.1 286 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	3308	Compositional matrix adjust.	11/20(55%)	14/20(70%)	0/20(0%)

```
Query  566  LFLFIVIFALLGMQLFGGRY  585
            L+LF+ +F LL   LFGG Y
Sbjct  89   LYLFLAVFPLLAALLFGGNY  108
```

No matches to hepatitis A, polio, measles, mumps, rubella, human influenza A or human papilloma viruses, in the first 10000 results.

Voltage-dependent L-type calcium channel subunit alpha-1D (CACNA1D)

Ion transport protein [Streptococcus pneumoniae]
CJK91097.1 279 2

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
71.2 bits(173)	3e-11	Composition-based stats.	57/266(21%)	119/266(44%)	55/266(20%)

```
Query  1207  FEYMMFVLIMLNTLCLAMQHYEQ-SKMFNDAMDILNMVFTGVFTVEMVLKVIAFKPKGYF  1265
                    F+  + +LI++N   L MQ       + +A+ +L+ +   VF  E+  ++   +   +F
Sbjct  22    FQRGILLLIVINAAILGMQTSAALVARWGEALVLLDSLILAVFVAEIAARIYVHR-AAFF  80

Query  1266  SDAWNTFDSLIVIGSIIDVALSEADPTESENVPVPTATPGNSEESNRISITFFRLFRVMR  1325
                      D W+ FD      S++ +AL           VP + P          +  R  RV+R
Sbjct  81    RDPWSLFDF-----SVVAIAL------------VPASGP----------FSILRALRVLR  113

Query  1326  LVKLLSRGEGIRTLLWTFIKSFQALPYVALLIAMLFFIYAVIGMQMFGKVAMRDNNQINR  1385
                     ++++++    +R ++   + +   L  +A+++A++F++ AVI   +F          +
Sbjct  114   VMRMVTMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAA---------DF  164

Query  1386  NNNFQTFPQAVLLLFRCATGEAWQEIMLACLPGKLCDPESDYNPGEEYTCGSNFAIVYFI  1445
                        F +  ++V  LF+  T E+W          +  P  +  P         +A V+FI
Sbjct  165   PEWFGSLGRSVYTLFQVMTLESWSM--------GIVRPVMEIFP---------YAWVFFI  207

Query  1446  SFYMLCAFLIINLFVAVIMDNFDYLT  1471
                      F ++  F ++NLF+A+I++    +T
Sbjct  208   PFILIATFTMLNLFIAIIVNAMQTVT  233
```

Cch1p [Saccharomyces cerevisiae YJM993]
AHY79558.1 2039 4

See 4 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
67.4 bits(163)	4e-09	Compositional matrix adjust.	74/287(26%)	120/287(41%)	48/287(16%)

```
Query  167   AFLIIFTVETFLKIIAYGLLLHPNAYVRNGWNLLDFVIVIVGLFSVILEQLTKETEGGNH  226
                    AF+  F++E  +K +A G +  PNAY+RN WN +DF ++I    S+ +  +      GN
Sbjct  1248  AFIGAFSIEFIVKTVADGFIYSPNAYLRNPWNFIDFCVLI----SMWINLIAYLKNNGNL  1303

Query  227   SSGKSGGFDVKALRAFRVLRPLRLVSGVPSLQVV--LNSIIKAMVPLLHIALLVLFVIII  284
                    S   G   + ALRA R L          +L +   LN I +A       L+ L ++
Sbjct  1304  SRIFKG---LTALRALRCLTISNTARQTFNLVMFDGLNKIFEA-------GLISLSLLFP  1353

Query  285   YAIIGLELFIGKMHKTCFFADSDIVAEEDPAPCAFSGNGR-QCTANGTECRSGW--VGP-  340
                    + + GL +F G++                C     GR  C    +     W  + P
Sbjct  1354  FTVWGLSIFKGRL----------GTCNDGSLGRADCYNEYSNSVFQWDIMSPR  1396
```

```
Query  341   --NGGITNFDNFAFAMLTVFQCITMEGWTDVLYWMNDAMGFELPWV--------YFVSLV  390
                                + D+FA A  +++Q I++EGW D+L  M ++ G   P         F+ L
Sbjct  1397  VYQQPYLHLDSFASAFNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVLF  1456

Query  391   IFGSF-FVLNLVLGVLSGEFSKEREKAKARGDFQKLREKQQLEEDLK  436
                     IF S  F+LNL + +   ++   A   + +  E Q+L   K
Sbjct  1457  IFLSMVFILNLFVSFIVNNQARTTGSAYFTIEEKAWLESQKLLSQAK  1503
```

polyprotein [Human hepatitis A virus]

APD15889.1 2227 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.2 bits(69)	457	Compositional matrix adjust.	20/74(27%)	38/74(51%)	8/74(10%)

```
Query  793  VNQIANSDNKVTIDDYREED--------EDKDPYPPCDVPVGEEEEEEEEDEPEVPAGPR  844
            +++IA  D + ++DD R E+         E ++PY    + VG++  +  ++E      P
Sbjct  767  MSRIAAGDLESSVDDPRSEEDKRFESHIECRNPYKELRLEVGKQRLKYAQEELSNEVLPP  826

Query  845  PRRISELNMKEKIA  858
            PR+I  L  + KI+
Sbjct  827  PRKIKGLFSQAKIS  840
```

large S protein, partial [Hepatitis B virus]

AGP15125.1 162 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
29.3 bits(64)	679	Composition-based stats.	17/55(31%)	25/55(45%)	1/55(1%)

```
Query  1716  PSIPPASDTEKPLFPPAGNSVCHNHHNHNSIGKQVPTSTNANLNNA-NMSKAAHG  1769
             P+ PP + T +PL+ PAG S         +    + +  + N N A NM   A G
Sbjct  89    PAAPPPASTNRPLYFPAGGSSSGTASPAQNTVSAISSILSKNGNPAPNMENIASG  143
```

DNA polymerase III subunits gamma and tau [Haemophilus influenzae 22.4-21]

EDK14149.1 688 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
26.9 bits(58)	7024	Compositional matrix adjust.	21/74(28%)	33/74(44%)	11/74(14%)

```
Query  1706  TTHRPLHVQRPSIPPASDTEKPLFPPAGNSVCHNHHNHN-SIGKQVPTSTNANL-----N  1759
             T  +P H+++P+ PP +        P  NS   N  + N  I +      +A+      N
Sbjct  472   TEPKPKHIEKPTSPPNAAQ-----APQKNSTEENSSDDNVEIAQDEQEILSADTYRWEWN  526

Query  1760  NANMSKAAHGKRPS  1773
             N  ++KA  G RPS
Sbjct  527   NPELAKADTGVRPS  540
```

bacterioferritin [Neisseria meningitidis]
WP_061725459.1 157 1

See 2 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	1133	Composition-based stats.	16/50(32%)	25/50(50%)	0/50(0%)

```
Query  2054  KQRSADSLVEAVLISEGLGRYARDPKFVSATKHEIADACDLTIDEMESAA  2103
             + ++AD L+E +L  EGL       K +     E   ACDLT ++ +  A
Sbjct  51    EMKAADDLIERILFLEGLPNLQELGKLLIGESTEEIIACDLTKEQEKHEA  100
```

ABC transporter permease, partial [Clostridium tetani]
KHO33579.1 71 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5827	Composition-based stats.	6/22(27%)	16/22(72%)	0/22(0%)

```
Query  1449  MLCAFLIINLFVAVIMDNFDYL  1470
             ++CA ++++L +  + DNF ++
Sbjct  37    IICALIVVHLLIPFVKDNFTHI  58
```

hypothetical protein [Bordetella pertussis]
WP_050849081.1 160 1

See 3 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.9 bits(63)	804	Composition-based stats.	8/16(50%)	9/16(56%)	0/16(0%)

```
Query  1981  WATPPATPPYRDWTPC  1996
             W  PPA+ P   W PC
Sbjct  133   WVLPPASSPTTSWIPC  148
```

hypothetical protein [Corynebacterium diphtheriae]
WP_010934020.1 86 1

See 3 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.8 bits(55)	4962	Composition-based stats.	14/43(33%)	24/43(55%)	3/43(6%)

```
Query  24  ANYARGTRLP---LSGEGPTSQPNSSKQTVLSWQAAIDAARQA  63
           A +A+ T L    L+GE P  QPN+ ++ V   + A+  + +A
Sbjct  2   ATHAQSTELLEALLAGEAPRFQPNTGQELVDDIEIALSPSARA  44
```

No matches to measles, mumps, rubella, polio, human papilloma or human influenza viruses, in the first 10000 results.

Voltage-dependent L-type calcium channel subunit alpha-1F (CACNA1F)

Cch1p [Saccharomyces cerevisiae YJM1399]
AJS28472.1 2039 5

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
146 bits(369)	3e-33	Compositional matrix adjust.	168/732(23%)	314/732(42%)	56/732(7%)

```
Query  847   EGSAFFCLSQTNPLRKGCHTLIHHHVFTNLILVFIILSSVSLAAEDPI-RAHSFRNHILG  905
                    +GS FF  S    ++    I  VF  +  +  IL  V     P+ R H   H +G
Sbjct  1182  DGSRFFEDSTDLYNKRSYFHHIERDVFVFIFALATILLIVCSCYVTPLYRMH----HKMG  1237

Query  906   YFDY------AFTSIFTVEILLKMTVFGAFLHRGSFCRSWFNMLD---LLVVSVSLISFG  956
                       +++     AF   F++E ++K   G     ++ R+ +N +D   L+ + ++LI++
Sbjct  1238  TWNWSSALDCAFIGAFSIEFIVKTVADGFIYSPNAYLRNPWNFIDFCVLISMWINLIAYL  1297

Query  957   IHSSAIS-VVKILRVLRVLRPLRAINRAKGLKHVVQCVFVAIRTIGNIMIVTTLLQFMFA  1015
                       ++  +S + K L  LR LR L   N A+   ++V  +F  +  I    +++  L F F
Sbjct  1298  KNNGNLSRIFKGLTALRALRCLTISNTARQTFNLV--MFDGLNKIFEAGLISLSLLFPFT  1355

Query  1016  CIGVQLFKGKFYTCTDEAKHTPQECKGSFLVYPDGDVSRPLVRERLWVNSDFNFDNVLSA  1075
                        G+ +FKG+  TC DE+    +C     Y +     ++  R++    + D+  SA
Sbjct  1356  VWGLSIFKGRLGTCNDESLGR-ADCYNE---YSNSVFQWDIMSPRVYQQPYLHLDSFASA  1411

Query  1076  MMALFTVSTFEGWPALLYKAIDAYAEDHGPIYNYRVEISVFFIVYIIIIAFFMMNIFVGF  1135
                        +L+ + + EGW  LL   +++            ++F +++  +   F++N+FV F
Sbjct  1412  FNSLYQIISLEGWVDLLENMMNSSGIGTPATVMGSAGNALFLVLFNFLSMVFILNLFVSF  1471

Query  1136  VIITFRAQGEQEYQNCELDKNQRQCVEYALKAQPLRRYIPK-----NPHQYRVWATVNSA  1190
                        ++        Y  E +K   +  +A+P  + IP        Q+    V
Sbjct  1472  IVNNQARTTGSAYFTIE-EKAWLESQKLLSQAKP--KAIPNLIELSRVRQFFYQLAVEKK  1528

Query  1191  AFEYLMFL--LILLNTVALAMQHYEQTAPFNYAMDILNMVFTGLFTIEMVLKIIAFKPKH  1248
                         F Y  FL  ++ L+ + L  + Y      Y   +  M  T +F I+  L +    P+
Sbjct  1529  NFYYASFLQVVLYLHIIMLLSRSYNPGNLIGY-QGVYFMFSTSVFLIQEALHMCGEGPRL  1587

Query  1249  YFTDAWNTFDALIVVGSIVDIAVTEVNNGGHLGESSEDSSRISITFFRLFRVMRLVKLLS  1308
                         YF   WN+    I++ + +  AV      H+  S     I      F ++  + ++
Sbjct  1588  YFRQKWNSIRLSIIIIAFIMNAV-----AFHVPASHYWFHNIK----GFFLLVIFLFIIP  1638

Query  1309  KGEGIRTLLWTFIKSFQALPYVALLIAMIFFIYAVIGMQMFGKVALQDGTQINRNNNFQT  1368
                         + + +  LL T + S   +  +    ++F +YA+   Q+FG   L  G+    N NF+T
Sbjct  1639  QNDTLTELLETAMASLPPILSLTYTWGVLFLVYAIALNQIFGLTRL--GSNTTDNINFRT  1696

Query  1369  FPQAVLLLFRCATGEAWQEIM---LASLPGNRCDPESDFGPGEEFTCGS-NFAIAYFISF  1424
                            +++++LFRC+ GE W  IM     S P    D  S +       CGS  +A    +S+
Sbjct  1697  VIKSMIVLFRCSFGEGWNYIMADLTVSEPYCSSDDNSTYT-----DCGSETYAYLLLMSW  1751

Query  1425  FMLCAFLIINLFVAVIMDNFDYLTR---DWSILGPHHLDEFKRIWSEYDPGAKGRIKHLD  1481
                         ++  ++ +N+FV++I+ NF Y+ R     S +    + ++   WS++D    G ++
Sbjct  1752  NIISMYIFVNMFVSLIIGNFSYVYRSGGSRSGINRSEIKKYIEAWSKFDTDGTGELELSY  1811
```

```
Query  1482  VVALLRRIQPPLGFGKLCPHRVACKRLVAMNMPLNSDGTVTFNATLFALVRTSLKIKTEG  1541
                   + ++    PL F K+   R+  K LV   M +N D      L  L +   I
Sbjct  1812  LPRIMHSFDGPLSF-KIWEGRLTIKSLVENYMEVNPDDPYDVKIDLIGLNKELNTIDKAK  1870

Query  1542  NLEQANQELRIV  1553
                +++ Q  R V
Sbjct  1871  IIQRKLQYRRFV  1882
```

Ion transport protein [Streptococcus pneumoniae]
CJK91097.1 279 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
53.1 bits(126)	2e-05	Compositional matrix adjust.	58/277(21%)	110/277(39%)	60/277(21%)

```
Query  861   RKGCHTLIHHHVFTNLILVFIILSSVSLAAEDPIRAHSFRNHILGYFDYAFTSIFTVEIL  920
              R      I    F   IL+ I++++  L  +      +     L   D    ++F  EI
Sbjct  10    RSRLGQFIERPAFQRGILLLIVINAAILGMQTSAALVARWGEALVLLDSLILAVFVAEIA  69

Query  921   LKMTVFGAFLHRGSFCRSWFNMLDLLVVSVSLISFGIHSSAISVVKILRVLRVLRPLRAI  980
               ++     ++HR +F R  +++ D  VV+++L+      S +  +++LRV+R+      +
Sbjct  70    ARI-----YVHRAAFFRDPWSLFDFSVVAIALVPASGPFSILRALRVLRVMRM------V  118

Query  981   NRAKGLKHVVQCVFVAIRTIGNIMIVTTLLQFMFACIGVQLFKGKFYTCTDEAKHTPQEC  1040
                   ++ VV  +  AI  +G+I +V  L+ ++ A I   LF   F
Sbjct  119   TMVPSMRRVVGALLSAIPGLGSIAMVLALVFYVSAVIATGLFAADF--------------  164

Query  1041  KGSFLVYPDGDVSRPLVRERLWVNSDFNFDNVLSAMMALFTVSTFEGWPALLYKAIDAYA  1100
                      P+            W      F ++  ++  LF V T E W   + +
Sbjct  165   -------PE-----------W------FGSLGRSVYTLFQVMTLESWSMGIVR------  193

Query  1101  EDHGPIYNYRVEISVFFIVYIIIIAFFMMNIFVGFVI  1137
                  P+        VFFI +I+I  F M+N+F+  ++
Sbjct  194   ----PVMEIFPYAWVFFIPFILIATFTMLNLFIAIIV  226
```

polyketide synthase [Corynebacterium diphtheriae]
WP_014308834.1 2639 1

See 1 more title(s)

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
28.5 bits(62)	2308	Compositional matrix adjust.	18/48(38%)	28/48(58%)	3/48(6%)

```
Query  1898  LVEAVLISEG--LGLFARDPRFVALAKQEIADACRLTLDEMDNAASDL  1943
              ++ A++  EG  L L A DP+ VA    E+ D C  T DE+D A +++
Sbjct  1867  MLRAIVTDEGHQLILDADDPQ-VATPPVEVVDLCDATADEVDQAITEV  1913
```

aminopeptidase, partial [Bordetella pertussis]
WP_055345188.1 253 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
34.7 bits(78)	20	Compositional matrix adjust.	18/46(39%)	22/46(47%)	0/46(0%)

```
Query  1170  LRRYIPKNPHQYRVWATVNSAAFEYLMFLLILLNTVALAMQHYEQT  1215
             +R+ I  NP    R W TVN    FE     L  +    A+A  HYEQ
Sbjct  128   IRQAIAANPEIGRAWPTVNPLVFECNDGYLNDIQAQAVAEAHYEQA  173
```

ABC transporter permease, partial [Clostridium tetani]
KHO33579.1 71 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
25.0 bits(53)	5220	Composition-based stats.	6/22(27%)	16/22(72%)	0/22(0%)

```
Query  1426  MLCAFLIINLFVAVIMDNFDYL  1447
             ++CA ++++L +  + DNF ++
Sbjct  37    IICALIVVHLLIPFVKDNFTHI  58
```

conserved hypothetical metabolite transport protein [Haemophilus influenzae PittHH]
EDK10412.1 344 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
31.2 bits(69)	298	Composition-based stats.	19/57(33%)	26/57(45%)	10/57(17%)

```
Query  717  MYDGIMAYGGPFFPGMLVCIYFIILFICGNYILLNVFLAIAVDNLASGDAGTAKDKG  773
            M + I  Y  PFF GMLVCI   +LF          ++ IA   + +  A T  + G
Sbjct  136  MLEVITTYFKPFFLGMLVCIAGYVLF----------YIMIAFSQIYAKSAPTVSEAG  182
```

hypothetical protein, partial [Neisseria meningitidis]
AEQ62062.1 327 1

GenPeptGraphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
27.7 bits(60)	3354	Composition-based stats.	17/44(39%)	23/44(52%)	2/44(4%)

```
Query  34  AVEGESSGASGLGTPKRRNQHSKHKT--VAVASAQRSPRALFCL  75
           A +G +  A  LG    +N H +     +  ASAQR P+ALF L
Sbjct  32  AEQGYTEAAFVLGNHLLQNGHPEQAFPWLETASAQRHPKALFTL  75
```

No matches to measles, mumps, rubella, polio, hepatitis A/B, human papilloma or human influenza A viruses, in the first 10000 results.

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